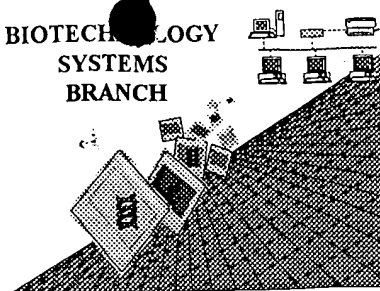


J. Keir

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



HAZ

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/327,750B
Source: 1633
Date Processed by STIC: 5/4/2001

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MAY 17 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

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<http://www.uspto.gov/web/offices/pac/checker>



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

CEA/FCE-1994

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/327,750	6/7/99	Taka-Aki Sato	0575/59131/JPW/APE

EXAMINER	
Janet M. Kerr	
ART UNIT	PAPER NUMBER
1633	13

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The communication, filed on 4/23/01, is non-responsive to the prior Office action, mailed 3/20/01, because of the following reason:

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR § 1.821 through 1.825 (see the attached Raw Sequence Listing Error Report). Failure to respond to this requirement may result in abandonment of the instant application.

Since the response appears to be *bona fide*, but through an apparent oversight or inadvertence failed to provide a complete response, applicant is required to complete the response within a time limit of one month from the date of this letter or as extended as follows. AN EXTENSION OF THIS TIME LIMIT MAY BE GRANTED UNDER EITHER 37 C.F.R. § 1.136(a) OR (b) UP TO A MAXIMUM OF SIX MONTHS.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center located in Crystal Mall 1. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989).

The CM1 Fax Center number is either (703)305-3014 or (703)308-4242.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Janet M. Kerr, Ph.D., whose telephone number is (703)305-4055.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Deborah Clark, can be reached at (703)305-4051.

Any inquiry of a general nature or relating to the status of this application should be directed to Patent Analyst, Kimberly Davis, whose telephone number is (703)305-3015.

DEBORAH J. R. CLARK
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/329,750B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

RECEIVED

MAY 17 2001

TECH CENTER 1600/2900

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☒ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) 6 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1633

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/327,750B

DATE: 05/04/2001
TIME: 16:34:33

p. 2

Input Set : A:\PTO.txt
Output Set: N:\CRF3\05042001\I327750B.raw

**Does Not Comply
Corrected Diskette Needed**

3 <110> APPLICANT: Sato, Taki-Aki
5 <120> TITLE OF INVENTION: GENE ENCODING NADE, P75NTR- ASSOCIATED CELL DEATH EXECUTOR AND USES
6 THEREOF
8 <130> FILE REFERENCE: 0575/59131/JPW/APE
10 <140> CURRENT APPLICATION NUMBER: 09/327,750B
11 <141> CURRENT FILING DATE: 1999-06-07
13 <160> NUMBER OF SEQ ID NOS: 45
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 36
19 <212> TYPE: DNA
20 <213> ORGANISM: MOUSE
22 <400> SEQUENCE: 1
23 aattgtctac gcataccttat gggggagctg tctaac 36
26 <210> SEQ ID NO: 2
27 <211> LENGTH: 12
28 <212> TYPE: PRT
29 <213> ORGANISM: MOUSE
31 <400> SEQUENCE: 2
33 Asn Cys Leu Arg Ile Leu Met Gly Glu Leu Ser Asn
34 1 5 10
36 <210> SEQ ID NO: 3
37 <211> LENGTH: 30
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <221> NAME/KEY: misc_feature
43 <222> LOCATION: (1)..(30)
44 <223> OTHER INFORMATION: Mouse Nade DNA
47 <400> SEQUENCE: 3
48 ctagctagca tcatggtgag caagggcgag 30
51 <210> SEQ ID NO: 4
52 <211> LENGTH: 28
53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <221> NAME/KEY: misc_feature
58 <222> LOCATION: (1)..(28)
59 <223> OTHER INFORMATION: Mouse Nade DNA
62 <400> SEQUENCE: 4
63 ccgctcgagt cttgtacagc tcgtccat 28
66 <210> SEQ ID NO: 5
67 <211> LENGTH: 29
68 <212> TYPE: DNA
69 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:
72 <221> NAME/KEY: misc_feature

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/327,750B

DATE: 05/04/2001
 TIME: 16:34:33

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\05042001\I327750B.raw

73 <222> LOCATION: (1)..(29)
 74 <223> OTHER INFORMATION: Mouse Nade DNA
 77 <400> SEQUENCE: 5
 78 atcctcgagc gatcatggcc aatgtccac
 81 <210> SEQ ID NO: 6
 82 <211> LENGTH: 27
 83 <212> TYPE: DNA
 C--> 84 <213> ORGANISM: Artificial Sequence
 W--> 86 <220> FEATURE:
 W--> 86 <223> OTHER INFORMATION:
 86 <400> SEQUENCE: 6
 87 atcggatcct ctacgtgta gctccct
 90 <210> SEQ ID NO: 7
 91 <211> LENGTH: 27
 92 <212> TYPE: DNA
 93 <213> ORGANISM: Artificial Sequence
 95 <220> FEATURE:
 96 <221> NAME/KEY: misc_feature
 97 <222> LOCATION: (1)..(27)
 98 <223> OTHER INFORMATION: Mouse Nade DNA
 101 <400> SEQUENCE: 7
 102 atcggatccg atctctctca tctcctc
 105 <210> SEQ ID NO: 8
 106 <211> LENGTH: 27
 107 <212> TYPE: DNA
 108 <213> ORGANISM: Artificial Sequence
 110 <220> FEATURE:
 111 <221> NAME/KEY: misc_feature
 112 <222> LOCATION: (1)..(27)
 113 <223> OTHER INFORMATION: Mouse Nade DNA
 116 <400> SEQUENCE: 8
 117 aaagcttagg gaggcacagc tgagaaa
 120 <210> SEQ ID NO: 9
 121 <211> LENGTH: 27
 122 <212> TYPE: DNA
 123 <213> ORGANISM: Artificial Sequence
 125 <220> FEATURE:
 126 <221> NAME/KEY: misc_feature
 127 <222> LOCATION: (1)..(27)
 128 <223> OTHER INFORMATION: Mouse Nade DNA
 131 <400> SEQUENCE: 9
 132 tttctcagct gtgcctccct aagcttt
 135 <210> SEQ ID NO: 10
 136 <211> LENGTH: 26
 137 <212> TYPE: DNA
 138 <213> ORGANISM: Artificial Sequence
 140 <220> FEATURE:
 141 <221> NAME/KEY: misc_feature
 142 <222> LOCATION: (1)..(26)

29

27

27

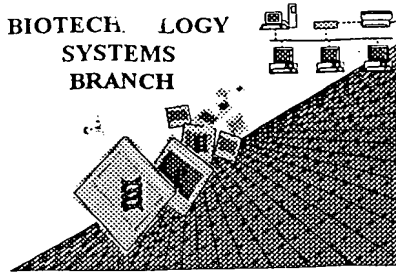
27

27

→ see item 12 on Error
 Summary
 sheet

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECH. LOGY
SYSTEMS
BRANCH



4/2

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/327,750B

Source:

1633

Date Processed by STIC:

5/4/2001

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MAY 17 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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Checker Version 3.0

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Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

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<http://www.uspto.gov/web/offices/pac/checker>

59131



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/327,750	06/07/99	Taka-Aki Sato	0575/59131/JRW/APW/AK

JOHN P WHITE
COOPER & DUNHAM LLP
1185 AVENUE OF THE AMERICAS
NEW YORK NY 10036

DOCKET CLERK
HZ1270601
1m. 7.1.01
2m. 8.1.01
3m. 9.1.01
4m. 10.1.01
5m. 11.1.01
6m. 12.1.01

EXAMINER	
Janet M. Kerr, I	
ART UNIT	PAPER NUMBER
1633	13
DATE MAILED:	

06/01/01

AP

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The communication, filed on 4/23/01, is non-responsive to the prior Office action, mailed 3/20/01, because of the following reason:

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR § 1.821 through 1.825 (see the attached Raw Sequence Listing Error Report). Failure to respond to this requirement may result in abandonment of the instant application.

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Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center located in Crystal Mall 1. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989).

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DEBORAH J. R. CLARK
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/329,250B

RECEIVED

MAY 17 2001

TECH CENTER 1600/2901

- ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
- 1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
 - 2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
 - 3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
 - 4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
 - 5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
 - 6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
 - 7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
 - 8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
 - 9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
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Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
 - 11 _____ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
 - 12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) 6 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
 - 13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.